IN THE SPECIFICATION:

Please amend the specification as follows:

Delete the Table of Contents, on pages i, ii, and iii.

Amend the paragraph beginning "Protein "spots"" which spans pages 32 and 33 to read as follows:

"Protein spots" that appear in samples from HSPR-positive membranes but are absent in samples from HSPR-negative membrane proteins can be analyzed further. Differences can be detected by visual inspection of gels, or by using densitometry and computerized image analysis thereby facilitating spot detection, background subtraction and spot matching (*see* Pennigton et al., 1997, Trends Cell Biol. 7: 168-73). Further, HSPR protein can be detected by Western Blot analysis of 2D gels, if HSPR antibody is available (Harlow and Lane, *supra*). Once identified, the molecular weight (M_r) and the isoelectric point (p*I*) of an HSPR-positive cell specific protein can be determined by calibrating its position relative to known standards run in parallel on 2D gels. Specific proteins can then be purified, and their sequence determined by Edman degradation sequencing (Edman and Begg, 1967, Eur. J. Biochem. 1:80-91), automated by electroblotting onto polyvinylidene difluoride (PVDF) membranes using Edman degradation chemistry determined by gas-liquid phase, liquid-pulse or solid phase sequence analysis (Findlay and Geisow, 1989, Protein Sequencing: A Practical Approach, IRL Press, Oxford, pp. 1-199). Alternatively, proteins and peptides can be characterized by mass spectrometry, using peptide-mass fingerprinting or protein sequencing methodologies to identify sequence information and post-translational modifications (Dainese et al., 1997, Electrophoresis, 18:432-42; Mann and Wilm, 1995, Trends Biochem. Sci., 20:219-24; Yates, 1996, Methods Enzymol. 271:351-77). After limited sequence information is obtained,

protein (Swiss-Prot) and nucleic acid sequence (Genebank and EMBL) databases can be searched to determine if protein sequence is novel. Novel proteins will be analyzed further in HSP binding assays, used to generate antibodies, as described in Section 5.4, and used for identification of HSPR nucleic acid sequences.

D1 cont.

Amend the paragraph beginning "In a preferred embodiment" which spans pages 44 and 45 to read as follows:

In a preferred embodiment, mRNA from HSPR positive is compared to mRNA from HSPR negative cells by differential display. HSPR positive cells and HSPR negative cells are prepared as described in Section 5.1, *supra*. The preparation of mRNA is as described in Section 5.5.1. Following RT-PCR using the specific set of primers described hereinabove, RT-PCR products are displayed on thin polyacrylamide gels containing 8% urea, the type used for DNA sequencing analysis. Products that are detected in HSPR positive cells but absent in HSPR negative control cells are chosen to be analyzed further. Gel purification and sequence analysis of such products can be performed to identify HSPR nucleic acid candidates. Protein-coding sequences of HSPR candidates, i.e., sequences present in HSPR positive cells but not in control cells, can be compared to known protein sequences in a data base such as Swiss-prot (Bairoch & Apweiler, 1998, Nucl. Acids Res. 26:38-42). Novel sequences can be chosen as potential HSPR candidates. Such gene products can then be isolated from the cDNA population using standard cloning techniques (Ausubel et al., 1992, supra), and can be tested for their ability to bind HSP ligand and antibodies.

D2

IN THE CLAIMS:

Please amend the claims as follows:

Cancel claims 52-54, 61, 62, and 74-76, without prejudice.

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